#2 (13)

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/028,748

DATE: 02/06/2002
TIME: 09:38:39

Input Set : N:\Crf3\RULE60\10028748.raw
Output Set: N:\CRF3\02062002\J028748.raw

ENTERED

SEQUENCE LISTING

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 1  (1) GENERAL INFORMATION:
 2       (i) APPLICANT: Mack, David H.
 3      (ii) TITLE OF INVENTION: COMPUTER-AIDED VISUALIZATION OF
 4                               EXPRESSION COMPARISON
 5     (iii) NUMBER OF SEQUENCES: 2
 6      (iv) CORRESPONDENCE ADDRESS:
 7           (A) ADDRESSEE: Joe Liebeschuetz of Townsend and Townsend and
 8                         Crew LLP
 9           (B) STREET: Two Embarcadero Center, Eighth Floor
10           (C) CITY: San Francisco
11           (D) STATE: CA
12           (E) COUNTRY: USA
13           (F) ZIP: 94111-3834
14       (v) COMPUTER READABLE FORM:
15           (A) MEDIUM TYPE: Floppy disk
16           (B) COMPUTER: IBM PC compatible
17           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
18           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
22      (vi) CURRENT APPLICATION DATA:
23           (A) APPLICATION NUMBER: US/10/028,748
24           (B) FILING DATE: 21-Dec-2001
25           (C) CLASSIFICATION:
28     (vii) PRIOR APPLICATION DATA:
29           (A) APPLICATION NUMBER: US/09/020,743
30           (B) FILING DATE: 09-Feb-1998
34    (viii) ATTORNEY/AGENT INFORMATION:
35           (A) NAME: Liebeschuetz, Joe
36           (B) REGISTRATION NUMBER: 37,505
37           (C) REFERENCE/DOCKET NUMBER: 018547034800US
38       (ix) TELECOMMUNICATION INFORMATION:
39           (A) TELEPHONE: (650) 326-2400
40           (B) TELEFAX: (650) 326-2422
41  (2) INFORMATION FOR SEQ ID NO: 1:
42       (i) SEQUENCE CHARACTERISTICS:
43           (A) LENGTH: 2691 base pairs
44           (B) TYPE: nucleic acid
45           (C) STRANDEDNESS: unknown
46           (D) TOPOLOGY: not relevant
47      (ii) MOLECULE TYPE: DNA (genomic)
48      (vi) ORIGINAL SOURCE:
49           (A) ORGANISM: Homo sapiens
50       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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C--> (lines 23, 24)
W--> (line 46)

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51    GGAGACAGAC AGACAGCTGG CAAGAGGCAG CCTGGGGGCC ACAGCTGCTT CAGCAGACCT    60
52    CATGGCTGAG TGAGCCTCCC CTGGGCCCAG CACCCCACCT CAGCATGGTC CAAGCCCATG    120
53    GGGGGCGCTC CAGAGCACAG CCGTTGACCT TGTCTTTGGG GGCAGCCATG ACCCAGCCTC    180
54    CGCCTGAAAA AACGCCAGCC AAGAAGCATG TGCGACTGCA GGAGAGGCGG GGCTCCAATG    240
55    TGGCTCTGAT GCTGGACGTT CGGTCCCTGG GGGCCGTAGA ACCCATCTGC TCTGTGAACA    300
56    CACCCCGGGA GGTCACCCTA CACTTTCTGC GCACTGCTGG ACACCCCCTT ACCCGCTGGG    360
57    CCCTTCAGCG CCAGCCACCC AGCCCCAAGC AACTGGAAGA AGAATTCTTG AAGATCCCTT    420
58    CAAACTTTGT CAGCCCCGAA GACCTGGACA TCCCTGGCCA CGCCTCCAAG GACCGATACA    480
59    AGACCATCTT GCCAAATCCC CAGAGCCGTG TCTGTCTAGG CCGGGCACAG AGCCAGGAGG    540
60    ACGGAGATTA CATCAATGCC AACTACATCC GAGGCTATGA CGGGAAGGAG AAGGTCTACA    600
61    TTGCCACCCA GGGCCCCATG CCCAACACTG TGTCGGACTT CTGGGAGATG GTGTGGCAAG    660
62    AGGAAGTGTC CCTCATTGTC ATGCTCACTC AGCTCCGAGA GGGCAAGGAG AAATGTGTCC    720
63    ACTACTGGCC CACAGAAGAG GAAACCTATG GACCCTTCCA GATCCGCATC CAGGACATGA    780
64    AAGAGTGCCC AGAATACACT GTGCGGCAGC TCACCATCCA GTACCAGGAA GAGCGCCGGT    840
65    CAGTAAAGCA CATCCTCTTT TCGGCCTGGC CAGACCATCA GACACCAGAA TCAGCTGGGC    900
66    CCCTGCTGCG CCTAGTGGCA GAGGTGGAGG AGAGCCCGGA GACAGCCGCC CACCCCGGGC    960
67    CTATCGTAGT CCACTGCAGT GCAGGGATTG GCCGGACGGG CTGCTTCATC GCCACGCGAA    1020
68    TTGGCTGTCA ACAGCTGAAA GCCCGAGGAG AAGTGGACAT TCTGGGTATT GTGTGCCAAC    1080
69    TGCGGCTAGA CAGAGGGGGG ATGATCCAGA CGGACGAGCA GTACCAGTTC CTGCACCACA    1140
70    CTTTGGCCCT GTATGCAGGC CAGCTGCCTG AGGAACCCAG CCCCTGACCC CTGCCACCCT    1200
71    CCGGTGGCCC AGGTGCCTAC CTCCCTCAAG CCTGGGAAGT CACAGGAAGC AGCAGCAGTA    1260
72    AGGACAAGGG GCCGGATTCC AGGTCTTCAA CACTGGCCAC TCCTCTGCTT CCTCTGTTGG    1320
73    CCCCAGATGG ACAGTAAGGG GAACCTCCAA TGTCTCTCTG AACTTAAAGA CAGGAGCTGG    1380
74    CATTTATGAC AGACAAAGAA AGAAGCCCAG GTGTCCTGGT GTTCTCTGAG ACACTCTTTG    1440
75    TGAGCTTCAG TTTCCTGTTC TATAACATGA ACATAAGTGC TTAGCTGCCA TGAGGGAAAA    1500
76    GTAATGAGAG AAGTTTCTAG AAGCCACTCC AGCCACTCCT TCCTGGGGCT GACAAAAGGG    1560
77    TGATTCCAAG ATCATCCTTC ACCCGAGGTC CTGCCCAAGC ACAGGCCAGA TGCAAGAATG    1620
78    GGGAAAGTC TGGTCCTGAT CTCCAAGTCT CAACATCCTA TCAGTGACTC TGCTCCCTGA    1680
79    CCACACATCG GAAGGGCTGG ATGACCCCAA TCAAAAGAAA GAACAAGGAC TCTGGTTACC    1740
80    CTTGCCCTCC ACCCATGTGT CATAAGAGTA GGCTACAGAG GTGACCAGGC CTGGCAGTTG    1800
81    AAATCTCTGG AAGAGGGAAC ATGTGGGGAC TACTCAGAGG CAAAGAGGAG CTGCTCCTGC    1860
82    CTCCATGGTT GCTGGCCACT CCCACCAACT ACTCTTAGGG AGGCTAAGCA GTCTCTGTTT    1920
83    TGCTTCCATG GCTCAAATAA TACCCTGGGT ATGCAGGACC CACTATACCT TGCATTTGCT    1980
84    GGTACACCTA GAGAGCTTGG CTGTTTCCAA AAACAATCAG GGTCATAACC ATCCATGCAG    2040
85    ACATGGAGGC TCGGCTGAAC CAGGACTCCT CACTGTCTAC CTGAGAGAAT GAGCACCCCT    2100
86    CATCCATCTC AGCATCAACA CAATTTCCAG GGGACCTCAG GTCTACCTCA GGACTGAACG    2160
87    CCACACCTCA GGATTCCTCC TCCTTGAATC TGAGACTGGC TGCCCATTCT GAGATGGGGA    2220
88    TGAAGGTAAG ATGCCGCATC ACCAGCACG CCGCCCCTGA CAGCTGCCTT GATACCAGCT    2280
89    CTCTGTGGAA ACCCCGAGG AGTTGGATCT GGAGAACAGC TGGGCCTCCT CACTCAGGAC    2340
90    TTCTCTCCTG AAGAACACGC AGTGCTAAAA CTGAGGATGA TTTCCCTAAT GCTTCTGCTT    2400
91    GGCCTTATGG AGGAGCTGCT CCTTCCTTAC AGCCTTGGGG ATGGACTTGC CCACACCTCC    2460
92    ACCTCCCCTG AGCCCTGTGA GAGGCACGAC TGTCTATGCC AATGAGGCTC GGTGGGGGGC    2520
93    TCTCAAGTGC CTGATCCTGC CCTGGGCTCA GAGCCAGCCC AGAGGGAAGC AACTGCACAG    2580
94    CCCCACAGGC CCTCCCTGGC ACTGTCCCCC CAACCCCATC TCAGAGCTCA GAGGGTACAA    2640
95    GCTCCAGAAC AGTAACCAAG TGGGAAAATA AAGACTTCTT GGATGACTGA C    2691
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97 (2) INFORMATION FOR SEQ ID NO: 2:
98   (i) SEQUENCE CHARACTERISTICS:
99   (A) LENGTH: 360 amino acids
100   (B) TYPE: amino acid

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```
        101              (C) STRANDEDNESS: not relevant
W--> 102              (D) TOPOLOGY: not relevant
        103       (ii) MOLECULE TYPE: protein
        104       (vi) ORIGINAL SOURCE:
        105              (A) ORGANISM: Homo sapiens
        106       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
        107              Met Val Gln Ala His Gly Gly Arg Ser Arg Ala Gln Pro Leu Thr Leu
        108              1               5                   10                  15
        109              Ser Leu Gly Ala Ala Met Thr Gln Pro Pro Glu Lys Thr Pro Ala
        110                          20                  25                  30
        111              Lys Lys His Val Arg Leu Gln Glu Arg Arg Gly Ser Asn Val Ala Leu
        112                          35                  40                  45
        113              Met Leu Asp Val Arg Ser Leu Gly Ala Val Glu Pro Ile Cys Ser Val
        114              50                      55                  60
        115              Asn Thr Pro Arg Glu Val Thr Leu His Phe Leu Arg Thr Ala Gly His
        116              65                      70                  75                  80
        117              Pro Leu Thr Arg Trp Ala Leu Gln Arg Gln Pro Pro Ser Pro Lys Gln
        118                              85                  90                  95
        119              Leu Glu Glu Glu Phe Leu Lys Ile Pro Ser Asn Phe Val Ser Pro Glu
        120                          100                 105                 110
        121              Asp Leu Asp Ile Pro Gly His Ala Ser Lys Asp Arg Tyr Lys Thr Ile
        122                          115                 120                 125
        123              Leu Pro Asn Pro Gln Ser Arg Val Cys Leu Gly Arg Ala Gln Ser Gln
        124                          130                 135                 140
        125              Glu Asp Gly Asp Tyr Ile Asn Ala Asn Tyr Ile Arg Gly Tyr Asp Gly
        126              145                 150                 155                 160
        127              Lys Glu Lys Val Tyr Ile Ala Thr Gln Gly Pro Met Pro Asn Thr Val
        128                              165                 170                 175
        129              Ser Asp Phe Trp Glu Met Val Trp Gln Glu Glu Val Ser Leu Ile Val
        130                          180                 185                 190
        131              Met Leu Thr Gln Leu Arg Glu Gly Lys Glu Lys Cys Val His Tyr Trp
        132                          195                 200                 205
        133              Pro Thr Glu Glu Glu Thr Tyr Gly Pro Phe Gln Ile Arg Ile Gln Asp
        134                          210                 215                 220
        135              Met Lys Glu Cys Pro Glu Tyr Thr Val Arg Gln Leu Thr Ile Gln Tyr
        136              225                 230                 235                 240
        137              Gln Glu Glu Arg Arg Ser Val Lys His Ile Leu Phe Ser Ala Trp Pro
        138                              245                 250                 255
        139              Asp His Gln Thr Pro Glu Ser Ala Gly Pro Leu Leu Arg Leu Val Ala
        140                          260                 265                 270
        141              Glu Val Glu Glu Ser Pro Glu Thr Ala Ala His Pro Gly Pro Ile Val
        142                          275                 280                 285
        143              Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Cys Phe Ile Ala Thr
        144                          290                 295                 300
        145              Arg Ile Gly Cys Gln Gln Leu Lys Ala Arg Gly Glu Val Asp Ile Leu
        146              305                 310                 315                 320
        147              Gly Ile Val Cys Gln Leu Arg Leu Asp Arg Gly Gly Met Ile Gln Thr
        148                          325                 330                 335
        149              Asp Glu Gln Tyr Gln Phe Leu His His Thr Leu Ala Leu Tyr Ala Gly
```

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```
150                   340              345            350
151           Gln Leu Pro Glu Glu Pro Ser Pro
152                   355              360
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VERIFICATION SUMMARY   DATE: 02/06/2002
PATENT APPLICATION: US/10/028,748   TIME: 09:38:40

            Input Set : N:\Crf3\RULE60\10028748.raw
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L:23 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:24 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:46 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:102 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2